Title: Identifying novel *R*-genes in rice wild relatives with microsatellite markers

Authors: G.C. Eizenga, H.A. Agrama, and F.N. Lee

Rice wild relatives (*Oryza* spp.) are an important source of novel *R*(resistance)-genes for rice improvement. Rice sheath blight, caused by *Rhizotonia solani*, and leaf blast, caused by *Magnaportha grisea*, are major fungal diseases of cultivated rice (*O. sativa*) in the USA and of irrigated rice worldwide. To identify novel resistance genes, approximately 50 accessions representing the species *O. alta*, *O. australiensis*, *O. barthii*, *O. glaberrima*, *O. glumapatula*, *O. latifolia*, *O. meridionolis*, *O. nivara*, *O. officinalis*, and *O. rufipogon*, were screened for reaction to *M. grisea* and *R. solani*. Ten different blast races, each represented by a single isolate of *M. grisea*, and a single isolate of *R. solani* were used in the greenhouse disease screening. These accessions were genotyped with approximately 200 SSR markers and data from 138 SSR markers used to conduct genetic distance and cluster analysis on these accessions with the *PowerMarker* program. Preliminary data indicated a close relationship between many *O. barthii*, *O. nivara* and *O. rufipogon* accessions, the progenitors of cultivated rice. One *O. nivara* accession clustered closely with five U.S. rice cultivars included for comparison. Clustering was more distant between U.S. cultivars and accessions of the remaining *Oryza* spp. that were not progenitor species. Associations between the aforementioned SSR markers and the disease reactions of the *Oryza* spp. accessions to blast races and sheath blight also were delineated using the *PowerMarker* program. Preliminary analysis with eight blast races identified 34 markers associated with two or more blast races. These associations will be used to identify the regions where novel *R*-genes are located. To date, six accessions are being backcrossed to adapted U.S. germplasm for mapping population development to further analyze the *R*-genes and to select germplasm useful to U.S. rice breeding programs.